Mount 18 number 8 novémber 1995 CODEN MOMIEE ISSN 0950-382X QH1-M7980 Actin-besed modify Salmonella invasión ? ABLE COPY

Salmonella typhimurium secreted invasion determinants are homologous to Shigella Ipa proteins

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## Summary

Salmonella typhimurium secreted proteins (Ssp) were previously implicated in epithelial cell invasion. Here we describe four genes (sspB, sspC, sspD, and sspA), located between spaT and prgH, which encode proteins of 63, 42, 36, and 87 kDa, respectively. These Ssp are homologous to Shigella flexneri secreted proteins IpaB, IpaC, IpaD and IpaA. A non-invasive mutant with a transposon insertion in sspC lacks Ssp of 87, 42 and 36 kDa. Complementation analyses show that sspC and sspD encode the 42 and the 36 kDa Ssp. while the 87 kDa Ssp is encoded by sspA. sspC and sspD, but not sspA, are required for invasion. Amino-terminal sequencing shows that SspC and SspA are secreted without amino-terminal processing. We further demonstrate that Ssp secretion requires proteins encoded by prgHIJK, homologous to the Shigella Ipa secretion system, since SspA is abundantly secreted by wild-type bacteria but is completely retained within the cellular fraction of a prgHIJK nutant. A precipitate containing abundant SspC and three other major Ssp of 63, 59 and 22 kDa was isolated from culture supernatants of wild-type bacteria. These data indicate that major secreted invasion determipants of S. typhimurium are structurally and functionally homolgous to S. flexneri lpa proteins.

## **giro**duction

number of enteroinvasive bacterial pathogens secrete fulence determinants which facilitate colonization of mammalian hosts and evasion of immunological efences (Bliska et al., 1993). Enteroinvasive Shigella

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Peceived 17 May, 1995; revised 6 March For correspondence. E-mail i 16 5107; Fax (206) 616 4295

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species secrete three proteins (lpaB, lpaC and lpaD) necessary for the invasion of non-phagocytic epithelial cells (Ménard et al., 1993), a process thought to allow bacteria to invade the basolateral surface of the intestinal epithelium and to spread from cell to cell within the intestine (Perdomo et al., 1994; Zychlinsky et al., 1994b). In addition, IpaB facilitates escape of the bacteria from the phagocytic vacuole (High et al., 1992) and induces apoptosis in macrophages (Zychlinsky et al., 1994a). The Yop proteins secreted by enteropathogenic Yersinia spp. have a wide variety of effects on host cells and have tyrosine phosphatase and serine/threonine phosphokinase enzymatic activities. Yops' exhibit cytotoxicity, inhibit bacterial phagocytosis by macrophages (Rosqvist et al., 1990), inhibit the macrophage antimicrobial oxidative burst (Bliska and Black, 1995) and suppress production of the cytokine TNFα by macrophages (Beuscher et al., 1995).

Although Yop and Ipa proteins are neither structurally nor functionally homologous, highly related machineries of a sec-independent type III secretory pathway (Van Gijsegem et al., 1993) are utilized by Yersinia and Shigella spp. for Yop and Ipa secretion (Groisman and Ochman. 1993; Straley et al., 1993). Homologues of this secretion: apparatus are not restricted to mammalian bacterial pathogens. They are also important to secretion of virulence factors by bacterial plant pathogens and to flagellar assembly by both Gram-negative and Gram-positive bacteria (Sha--piro, 1995; Van Gijsegem et al., 1995). The Shigella flexneri (mxi and spa) and Yersinia spp. (ysc) genes that encode this secretion apparatus are localized on large virulence plasmids (Forsberg et al., 1994; Sasakawa et ... al., 1992). The Yop and Ipa proteins lack typical signal sequences and utilize additional factors, which may function as chaperones, for their secretion and/or presecretory stabilization. A number of Yops each require an individual chaperone for their secretion (Wattiau et al., 1994). In contrast, IpaB and IpaC are associated with a single small cytoplasmic chaperone, lpgC, which protects these proteins from intracellular degradation. After secretion, IpaB and lpaC form a complex which contains an additional 72 kDa protein, probably lpaA, with unknown function (Ménard et al., 1994b). In addition, IpaB and IpaD have been shown to transiently interact in the harmy brane. It has t ite Ipa secretion upon Nonth— QHI
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